

## SEQUENCE LISTING

- <120 \* Modified G-Protein Coupled Receptors</pre>
- <130 + 033072-026</pre>
- -:140 US 09/993,344
- <141 · 2001-11-05</pre>
- +:15: + US 60'245,772
- +:151.+ 2000-11-03
- -130- US 60/260,363
- -1151 2001-01-08
- ·\*160 \*\* 81
- \*1773 FastSEQ for Windows Version 4.0
- <210> 1
- <211> 371
- <212> PRT
- <213> Artificial Sequence
- $e^{\frac{1}{2}} \supseteq \mathbb{E}\left( \mathbb{C}^{n} +$
- <!i33 amino acid sequence of wild-type V2R</pre>
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- Met Leu Met Ala Ser Thr Thr Ser Ala Val Pro Gly His Pro Ser Leu : 10 10 15

  Pro Ser Leu Pro Ser Asn Ser Ser Gln Glu Arg Pro Leu Asp Thr Arg 20 25 30
- Asp Pro Leu Leu Ala Arg Ala Glu leu Ala Leu Leu Ser Ile Val Phe 35 40 45
- Mal Ala Val Ala Leu Ser Asn Gly Leu Val Leu Ala Ala Leu Ala Arg 50 55 60
- Arg Gly Arg Arg Gly His Trp Ala Pro Ile His Val Phe Ile Gly His
- 65 70 75 40 Deu Cys Leu Ala Asp Leu Ala Val Ala Leu Phe Gin Val Leu Fro Gin 85 90 75
- Leu Ala Trp Lys Ala Thr Asp Arg Phe Arg Gly Pro Asp Ala Leu Cys 100 105 110
- Arg Ala Val Lys Tyr Leu Glr Met Val Gly Met Tyr Ala Ser Jer Tyr 115 120 125
- Met Ile Leu Ala Met Thr Leu Asp Arg His Arg Ala Ile Cys Arg Pro 130 135 140
- Met Leu Ala Tyr Arg His Gly Ser Gly Ala His Trp Asn Arg Fro Val 145 150 185 186
- Led Val Ala Try Ala Phe Ser Led Led Led Ser Led Fro Glin Led Fhe 185 175

COPY OF PAPERS ORIGINALLY FILES

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lle Phe Ala Gin Arg Ash Val Glu Gly Gly Ser Gly Val Thr Asp Cys
            150
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Irp Ala Cys Phe Ala Glu Pro Trp Gly Arg Arg Thr Tyr Val Thr Trp
                             200
        195
Ile Ala Leu Met Val Phe .al Ala Pro Thr Leu Gly Ile Ala Ala Cys
                         215
Gln Val Leu Ile Phe Arg Glu Ile His Ala Ser Leu Val Pro Gly Pro
                                         235
                     230
Jer 311 Arg Pro Gly Gly Arg Arg Arg Gly Arg Arg Thr Gly Ser Pro
                                     250
Gly Glu Gly Ala His Val Ser Ala Ala Val Ala Lys Thr Val Arg Met
            260
                                 265
Thr Leu Val Ile Val Val Val Tyr Val Leu Cys Trp Ala Fro Phe Phe
                                                 285
                             280
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Leu Val Glr. Leu Trp Ala Ala Trp Asp Pro Glu Ala Pro Leu Alu Gly
                        295
Ala Pro Phe Val Leu Leu Met Leu Leu Ala Ser Leu Asn Ser Cys Thr
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Ash Pro Trp Hie Tyr Ala Ser Phe Ser Ser Ser Val Ser Ser Slu Leu
                                     330
                325
Arg Ser Leu Leu Cys Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly
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                                345
            340
Fro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp
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Thr Ser Ser
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- -112> PRT
- +2135 Artificial Sequence
- · . .2(i| ·
- +\_23- amino acid sequence of wild-type beta2AR
- i)(y.
- Met Gly Gln Pro Gly Asn Gly Ser Ala Phe Leu Leu Ala Fr: Asn Arg
- : Fr Hi≳ Ala Pro Asp His Asp Val Thr Gln Gln Arg Asp Glu Val Trp 20 25 35.
- Tal Mai Gly Met Gly Ile Mal Met Per Leu Ile Mal Leu Ala Ile Mal
- Fig. 317 Ash Val Leu Val Ile Thr Ala Ile Ala Lys Phe 310 Arg Leu 30 60
- G.n The Val The Ash Tyr Phe Ile The Ser Leu Ala Cys Ala Asp Leu n 70 75 80
- Mal Met Gly Leu Ala Val Val Pro Phè Gly Ala Ala His Ile Leu Met 85 90 et
- Dws Met Trp Thr Phe Gly Asn Phe Trp Cys 3lu Phe Trp Thr Jer Ile
- A p Va. Leu Cys Val Thr Ala Ser IIe Giu Thr Leu Cys Val IIe Alâ 115 - 120 - 125
- Mal Asp Arg Tyr Phe Ala ile Thr Ser Erd Phe Lys Tyr Bin Ser Leu 130 145
- Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val 145 - 150 - 169

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Ser Gly Leu Thr Ser Phe Leu Pro 11e Gln Met His Trp Tyr Arg Ala
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Thr His Gln Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
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Phe Phe Thr Ash Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
                         200
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                                            205
Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Gln
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                     215
Glu Ala Lys Arg Gln Leu Gln Lys Ile Asp Lys Ser Glu Gly Arg Phe
235 235 235
His Val 31r. Ash Leu Ser Gln Val Glu 31n Asp Gly Arg Thr Gly His
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Bly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
                                                270
           260
                             265
Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro
                         280
                                            285
Phe Phe Ile Val Ash Ile Val His Val Ile Glr. Asp Ash Leu Ile Arg
                                        390
                     295
Lys Glu Val Tyr lle Leu Leu Asn Trp lle Gly Tyr Val Asn Ser Gly
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                                    315
Phe Ash Pro Leu Ile Tyr Cys Ard Ser Pro Ash Phe Ard Ile Ala Phe
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                                 330
Gin Glu Leu Leu Dys Leu Arg Arg Ser Jer Leu Lys Ala Tyr Gly Ast
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Gly Tyr Ser Ser Asn Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val
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Glu Gln Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr
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                     375
Glu Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp
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                                     395
der Gln Gly Arg Ash Cys Ser Thr Ash Asp Ser Leu Leu
· 110. · 3
.:11 - 370
-.112 - FRT
```

The Phe Hy Ash Phe Trp

The Gla Bhe Try Thr Jee Ile

<sup>1.13</sup> Artificial Sequence

<sup>· 220 ·</sup> 

<sup>+123 -</sup> amino acid sequence of beta2-AR-V2R chimera

<sup>-400 - 3</sup> 

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Asp Mål Leu Cys Mal Thr Ala Ser Ile 31: Thr Leu Cys Mal Ile Ala

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125
                            120
Val Asp Arg Tyr Phe Ala Ile Thr Ser Pro Phe Lys Tyr Gln Ser Leu
                        135
                                           140
Leu Thr Lys Asn Lys Ala Arg Val Ile Ile Leu Met Val Trp Ile Val
                                       155
                   150
Ser Gly Leu Thr Ser Phe Leu Pro Ile Gln Met His Trp Tyr Arg Ala
                165
Thr His Glr Glu Ala Ile Asn Cys Tyr Ala Asn Glu Thr Cys Cys Asp
           190
                               185
Phe Phe Thr Asn Gln Ala Tyr Ala Ile Ala Ser Ser Ile Val Ser Phe
                          200
                                                205
Tyr Val Pro Leu Val Ile Met Val Phe Val Tyr Ser Arg Val Phe Glr.
    210
                       215
Glu Ala Lys Arg Glr Leu Gln Lys Ite Asp Lys Ser Glu Gly Arg Phe
His Wal Gin Ash Lou Ser Gin Val Glu Gin Asp Gly Arg Thr Mly His
               240
                                    2.50
Gly Leu Arg Arg Ser Ser Lys Phe Cys Leu Lys Glu His Lys Ala Leu
            2.50
                                265
Lys Thr Leu Gly Ile Ile Met Gly Thr Phe Thr Leu Cys Trp Leu Pro
                            .281
Phe the Tie Mai Arm Tie Mai His Mai Tie Gim Asp Asm Leu Tie Arg
                        2.95
Lys Olu Val Tyr lie Leu Leu Asm Trp Ile Gly Tyr Val Asm Fer Gly
                                        315
305
                    310
Phe Asn Pro Leu Ile Tyr Cys Arg Ser Fro Asp Phe Arg Ile Ala Phe
                                   330
               325
Gin Glu Leu Leu Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro
           340 345
Gin Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr
                            3.50
Ser Ser
   ÷70
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<211. 382
KB12H PRT
<2130 Artificial Sequence
~2201.
<223 - amino acid sequence of MOR-TAR chimera expressed</p>
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leu Ala Gln Ala Ser Cys Ser Pro Ala Pro Gly Ser Trp Leu Ast. Leu
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Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser iro Ser
Met Hal Thr Ala 110 Thr 110 Met Ala Lei Tyr Per 11e Val Hys Val
van dry hed fine dry Asmaine bed valuter Tyr Val Tie Mai Ard Tyr
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Thr Lys Met Lys Thr Ala Thr Ash Ile Tyr Ile Phe Ash Leu Ala Leu
                              105
                                                110
           100
Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Ash Tyr
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Leu Met Gly Thr Trp Pro Fhe Gly Thr Ile Leu Cys Lys Ile Val Ile
                      135
                                         140
Sur lie Asp Tyr Tyr Ash Met Phe Thr Ser lie Phe Thr Leu Cys Thr
                  150
                                     155
Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu
              165
                              170
Asp The Arg Thr Pro Arg Asr Ala Lys Ile Val Asr Val Cys Asn Trp
               185
lle Lei Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr
       195
                          200
Lys Tyr Arg Gir Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Fro
                      215
                                         220
Thr Trp Tyr Trp Glu Asn Lea Lea Lys Ile Cys Val Phe Ile Phe Ala
                                      235
                  230
Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Sly Leu Met Ile
                                 250
heu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
                             265
Ard Ash Leu Ard Ard Ile Thr Ard Met Val Leu Val Val Val Ala Val
                                             285
   275
                          280
Phe Ile Val Cys Trp Thr Pro IIe His Ile Tyr Val Ile Ile Lys Ala
 290
                      295
Leu Ile Thr Ile Pro Glu Thr Thr Phe Glr Thr Val Ser Trp His Phe
                                     315
                  310
Cys lle Ala Leu Gly Tyr Thr Asr. Ser Cys Leu Asn Pro Val Leu Tyr
                   330 335
              325
Ala Fhe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ala
                             345
           3.40
Ala Ala Arq Gly Arg Thr Pro Pro Ser Leu Gly Pro Glr Asp 31u Cer
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lys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
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1.1101 5
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<210% 5
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<212 PRT
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2213 - Artificial Dequence

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%.23 \* Amino acid sequence of LIAR-V.P. %imera expressed
 from the pEArrB-1/EIAR vestor

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                                                          8.0
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Ala Val Ala Glu Ile Ala Gly Phe Trp Pro Phe Gly Ser Phe Cys Asn
The Trp Val Ala Phe Asp He Met Cys Ser Thr Ala e. The Log Ask
           1.00
                               105
Leu Cys Val Ile Ser Val Asp Arg Tyr Trp Ala Ile Ser Ser Fro Phe
                           120
       115
Gln Tyr Glu Arg Lys Met Thr Pro Lys Ala Ala Phe Ile Leu Ile Ser
                       135
                                          140
  130
Val Ala Trp Thr Leu Ser Val Leu Ile Ser Phe Ile Pro Val Gln Leu
                  150
                                      155 160
Ser Trp His Lys Ala Lys Pro Thr Trp Pro Leu Asp Gly Asn Phe Thr
                                   17]
              1€5
Ser Leu Glu Asp Thr Clu Asp Asp Ash Cys Asp Thr Arg Leu Ser Arg
                               185
                                                   190
           180
Thr Tyr Ala Ile Ser Ser Ser Leu Ile Ser Phe Tyr Ile Pro Val Ala
       195
                           200
The Met The Val Thr Tyr Thr Ser The Tyr Arg The Ala Glm Lys Glm
                       215
                                          220
Ile Arg Arg Ile Ser Ala Leu Glu Arg Ala Ala Val His Ala Lys Asr.
                   23.0
                                      235
Cys Gln Thr Thr Ala Gly Ash Gly Ash Pro Val Glu Cys Ala Gln Sor
                                  250
               245
Glu Mer Ser Phe Lys Met Ser Phe Lys Arg Glu Thr Lys Vai Lea Lys
           260
                               265
                                                  270
Thr Let Ser Val Ile Met Gly Val Phe Val Cys Cys Trp Let Pro Phe
                       280 285
Phe Ile Ser Asn Cys Met Val Pro Phe Cys Gly Ser Glu Glu Thr Gln
                       295
Pro Phe Cys Ile Asp Ser Ile Thr Phe Asp Val Phe Val Trp Phe Gly
                                       315
                   310
305
Trp Ala Ash Ser Ser Leu Ash Pro Ile Ile Tyr Ala Phe Ash Ala Asp
                                   331
               3.:5
Phe Glr Lys Ala Phe Ser Thr Leu Leu Gly Cys Tyr Arg Leu Cys Ala
           340
                               345
Ala Ala Arg Sly Arg Thr Pro Pro Ser Leu Sly Pro Sln Asp Slu Ser
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Cys Thr Thr Ala Ser Ser Jer Leu Ala Lys Asp Thr Ser Ser
                       375
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<211 · 451
<212 · PRT
<213 · Artificial Jequente
<223 - amino acid sequence of 5HT1AR-V2R chimera
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Ala Fro Ene 31: Thr 31y 91y Ash In: Thr 31y 11e Ger Asp Val Thr

tal Ner Tyr (in th. 110 Thr Ner Lea Lyn Lea Ty Thr Lea 110 The

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Cys Ala Val Leu Gly Asn Ala Cys Val Val Ala Ala Ile Ala Lei Blu
                     5.5
   50
Arg Ser Leu Gln Asn Val Ala Asn Tyr Leu Ile Gly Ser Leu Ala Val
                  70
65
Thr Asp Leu Met Val Ser Val Lou Val Jen Pro Met Ala Ala Leu Tyr
                                 90
31r. Wal Leu Asn Lys Trp Thr Leu Gly Gln Val Thr Cys Asp Leu Phe
                            105
          100
Ile Ala Leu Asp Val Leu Cys Cys Thr Ser Ser Ile Leu His Leu Cys
                       120
                                           125
   115
Ala Ile Ala Leu Asp Arg Tyr Trp Ala Ile Thr Asp Pro Ile Asp Tyr
                           140
                  135
Val Asn Lys Arg Thr Pro Arg Arg Ala Ala Ala Leu Ile Ser Leu Thr
    180 155
Trp Leu Ile Gly Phe Leu Ile Ser Ile Pro Pro Met Leu Gly Trg Arq
                                170
              165
Thr Pro Glu Asp Ard Ser Asp Pro Asp Ala Cys Thr Ile Ser Lys Asp
                             135
          180
His Gly Tyr Thr Ile Tyr Ser Thr Phe Gly Ala Phe Tyr Ile Fro Leu
                      250
       195
Leu Leu Met Leu Val Leu Tyr Gly Arg Ile Phe Arg Ala Ala Arg Phe
Arg Ile Arg Lys Thr Val Lys Lys Val Glu Lys Thr Gly Ala Asp Thr
                  230
                                    235
225
Ard His Gly Ala Ser Pro Ala Fro Glr. Pro Lys Lys Ser Val Ash Gly
                                250
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Gld Ser Gly Ser Arg Asn Trp Aig Leu Gly Val Glu Ser Lys Ala Gly
                            265 270
   260
Gly Ala Leu Cys Ala Asn Gly Ala Val Arg Gln Gly Asp Asp Gly Ala
   275 240 285
Ala Leu Glu Val Ile Glu Val His Arg Val Gly Asn Ser Lys Glu His
                      295
                                        300
   290
Let Fro Let Pro Ser Glu Ala Gly Pro Thr Pro Cys Ata Fri Act Sor
                  31:
305
Phe Glu Arg Lys Ash Glu Arg Arm Ala Tlu Ala Lys Ard Lys Met Ala
              325
                                330
Leu Ala Arg 3.4 Phe Lys Thr Val Lys Thr Leu Gly lie Ile Met Gly
                             345
          3 ::-)
Thr Phe Ile Leu Cys Trp Leu Pho Phe Phe Ile Val Ala Leu Val Leu
                         3-46
                                            365
Pro Phe Cys Glu Ser Ser Cys His Met Pro Thr Leu Leu Gly Ala lle
                      376
                                        320
lle Asn Trp Des Bly Tyr Jer A n der Les Les Asn Fro Mal De Tyr
                                    3.95
365
Ala Tyr Ene Ast Lys Asp Fho Gin Ash Ala Fho Lys Lys IIA 115 Lys
Cys Asn Phe Cys Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly
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Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Leu Alw Lyw Asp
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Thr Jer Ser
   450
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<217> 7 <211> ±94 <2120 PRT

<213> Artificial Sequence

<2200

<223> amino acid sequence of beta3AR-V2R chimera expressed from pEArrB-1/beta3AR vector

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Der Der der Les Ala Lys Asp Thr Ser Der

385 390

-1210 - 8 - .11 - 362

-1212 - PRT

·213 · Artificial Sequence

· 320.

+223> amino acid sequence of Edg1R-V2R chimera expressed from pEArrB-1/Edg1R vector

· 4000 8

Met Gly Pro Thr Ser Val Pro Leu Val Lys Ala His Arg Ser Ser Mal

Ser Asp Tyr Val Ash Tyr Asp Ile Ile Val Arg His Tyr Ash Tyr Thr 30

Gly Lys Leu Asn Ile Ser Ala Asp Lys Glu Asn Ser Ile Lys Leu Thr 40

Ser Val Val Phe Ile Leu Ile Cys Cys Phe Ile Ile Leu Glu Asn Ile

Fhe Val Leu Leu Thr Ile Trp Lys Thr Lys Lys Phe His Arg Pro Met 75 70

Tyr Tyr Phe Ile Gly Asn Leu A.a Leu Ser Asp Leu Leu Ala Gly Val 3.5 90

Ala Tyr Thr Ala Asn Leu Leu Leu Ser Gly Ala Thr Thr Tyr Lys Leu  $1 \odot 5$ 100

Thr Frc Ala Gln Trp Phe Leu Arg Glu Gly Ser Met Phe Val Ala Leu 120125

Ser Ala Ser Val Phe Ser Leu Leu Ala Ile Ala Ile Glu Arg Tyr Ile 135 140

Thr Met Leu Lys Met Lys Leu His Ash Gly Ser Ash Ash Phe Arg Leu 155 150

Phe Leu Leu Ile Ser Ala Cys Trp Val Ile Ser Leu Ile Leu Gly Gly 170

Leu Pro Ile Met Gly Trp Asn Cys Ile Ser Ala Leu Ser Ser Cys Ser 1 - 5

Thr Val Leo Pro Leo Tyr His Lys His Tyr Ile Leo Phe Cys Thr Thr 300 195 205

Mal Phe Thr Leu Leu Leu Ser Ile Wal Ile Leu Tyr Cys Arg Ile 215

Tyr Ser Leu Mal Arg Thr Arg Ser Ang Arg Leu Thr Phe Arg Lys Asn 125 - 235 - 246

lle der bys Ala Ser Arg Ser Ser Siu bys Ser bet Ala bet bet bys 245 250

Thr Val lie lle Val Leu Ser Val Phe lle Ala Cys Trp Ala Fro Leu 260 265

Phe Ile Leu Leu Leu Asp Val Bly Cys Lys Val Lys Thr Cys Asp 280

ise Lew Phe Arg Ala Glu Tyr Phe Leu Val Leu Ala Val Leu Asn Ser 395

Bly Thr Ash Pro Ile Ile Tyr Thr Leu Thr Ash Lys Glu Met Arg Arg 310 315 305

Ala Phe Ile Arg Ile Met Ser Cys Cys Lys Cys Ala Ala Ala Arg Sly 330 325

Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Glu Ser Cys Thr Thr Ala 349 345

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4211 · 1113
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3213 - Artificial Sequence
-:22Ji-
+2233 nucleotide sequence of beta2AR-V2R chimera
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t stoloatny teotygopat ogtytttyge aatytyptyg teätoacaj mattyppaag 180

    dagagagte tgeagaeggt caccaastae tteatsaett cactggeefil tgetgatetg 240

urmatigges tygsagtiggt gesetttiggi geogessata tisttatuas satigtiggast 300

    thomsaast totggtgoga gttttggadt todattgatg tgotgtgog; hanggodago 360

strigagacco tigtigogtigat ogdagtiggat ogdtabtttig odattabit; mostiticaag 420
tabcagagos igotgacsaa gaataaggos egggtgatoa tibigatqui itiggatigig 4%1
traggootta ootoottott goodattoag atgeastggt acogggedan mäccaggaa 540
questicaact getatgecaa tgagacetge tgtgaettet teaegaac.W ugeetatgee 600
Attigestett seategtigte ettetaegtt decetiggtiga teatiggtett (gtetaetee 660
aymgtottto aggaggodaa aaggoagoto dagaagattg adaaatotga jygoogotto 720
matighocaga accittagoca ggtggagcag gatgggcgga cggggcatgg actoogcaga 780^\circ
tottobaagt totgottgaa ggagdadaaa goodtdaaga ogttaggdat batdatgggd 840
actiticacco teligologici geocticite alegitiaaca tigligeatgi galocaggal 900
aacctcatcc gtaaggaagt ttacatcctc ctaaattgga taggetatgt caattctggt 960
ticaatcood tiatetacig coggagoeda gatticagga tigoottoca ggagottoig 1020
tycycloggy gaeglaesee alsoeagesty gyteoscaay atgagteety raccalleges.
aquicotoco tggocaagga cacticatog tga
+311 + 10
11:11 - 1149
KILL - DNA
421: - Artificial Sequence
<2 3 - nucleotide sequence of MOR-V2R chimera</pre>
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atificages gradegace agggadess agradetant ragades to similarina \epsilon \delta
agit sotoob Hagbabotgg otbotggbth wastigtbus Angitish se seessa this 120
gardbatgog gtotgaabeg dabogggott ggogggaabg ahagbots, i himbagabb led
ggualosott esatggtsac agscattace ateatggede tetaetpprox x^{-1}unigtgtgta 240
gtygysotot toggaaastt ootggtoatg tätgtgattg taagataca: 33aaatgaag 301
actyroacca abatetacat tittoaacett getotggbag abgoottag: {appagtaca 868
otyphotitic agagitateas of accigate grassatege controppesh relabilities 42%
aagatogtga totoaataga ttaotabaad atgttbabba gbatattbar initotgbabb 480
atgamogtgg acogetaeat tgetgtetge cadecagtea aagecetgga iiteegtaee 540
recognishing graduaters caucatotyc auctogates totottotych mategatety 600 entytaangt transgraden nacaaaatan aggoagygyt chatagant massochaby 660
triptochain neachdagta chaggsaasc manthaseach matgrinn na btinch
nh sàitean an Insancethnair lean san sa mhaigh a nghitachagh ningaitgan mhí la calaist Salag <sup>ma c</sup>
ayuqttoyna tyitasiyyy itobaaaqaa aaygabadga atbiqoyray yatbabhogg 840
```

Faue 1

atygtgotig i gtograph igtathtafir gritgofgya combhafira Hatotangto 950

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gaaaacttba agcgatgott bagagagtto tgbyoggbby bacggggacg bacbcbabbo 108\%
agostgggto occaagatum gtootgcado accycoagot cotocotggo caaggacact 1140
                                                                      1149
toatogtga
< 10 \times 11
4711 - 1143
+.12 + DNA
+213 + Artificial Sequence
. . . . . .
+123> nubleotide sequence of DIAR-V2R chimera
+400 + 11
atygoteeta acaettetas patygatyay yooyyyotyo bayoyyayay yyattictoo 60.
titiografies transground titiostytical styrication tytiosactict potyggical 1.\,^{\circ}
accomplete grandscape categogeth ogsescongs gatocsaggt gadosactto 1% (
tiligicator ottbagorgi groagatore tiggiggorg teological geoorggaaa 240
getgtggoog agattgotgg ottittggood tittgggtoot tittgtaabat otgggtagoo 50%
titigabatba tigitgototab ggogtobatt otgaabbiot gogtgatbag ogtggabagg 🦫 🖰
tachyggista tistocagoos tittocaytat yayayyaaya igacccccaa aycayootto 🐍 🛚
atootgatta gogtagoaty gaototytot ytoottatat oottoatood agtabagota 48\%
aqotigoada aggbaaagoo babatigoobo tiiggatigoa attitabbib botigoaggad^{\circ}54^{\circ}
anogaggang acaactytya babaagytty agcaggabyt atycoattto atoytoocto 60^\circ
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gouragaagu aaaboggogo atotoagoot tggagagggo agcagtobat godaagaatt 71/
gebagaccae ogcaggitaae gggaaccceg tegaatgege ocagitetgaa agitteetitta 780
agatgtoott baagagggag abgaaagtto taaagabgot gtotgtgato atgggggtgt 840
thytytycty atygetesat thatteatet sydaactytat gytyseatta tytyyatety 900
aggagaccca gocattotgo atogattoca toacottoga tytytttyty tyytttyygt 960
gggogaatte ttoootgaab oobattatti atgotttaa tgotgabtto oagaaggõgt 10.0
totoaacoot oftaggatgo tacagactof goyoggoogo acggggacgo accocaccoa 10-0
postaggico ocaagatgag tootgoacca cogocagoto otocciggoo aaggabactt 1140
batogtiga.
+0.10 \cdot 12
\pm 3.11 \pm 1356
4012 - DNA
<:213 · Artificial Sequence</pre>
40023
<223 - misleptide sequence of SHTIAR-V2R chimera</p>
4.13(1) 1.2
atymatytys toagosotyg toaggybaab aabassasat bassasogys toostttyag 6\%
appgypggsa ababtaetgg tatetoogab ytyaboytea yotabeaayt gateabetet 13.)
stystystyg geasgeteat ettetgegeg gtystgygea atgegtgegt ggtggetgee 1\%
atogrottgg agogotoost goagaacgtg godaattato ttattggoto tttggoggto 240
appgapetea tygtgtoggt getggtgetg repatggoog bgetgtafda gytgetcaac 300
aagtiggabad tyggdbaggt aadotgbgab styttdatog bootdgabgt matytystyd 300
acotoatoba tottgoacot gtyogobato gogotggaba ggtastgyg: www.dulygab 4.
cocatogast asgigaadaa gaggadgood sgysgogoog sigsgoidat stigstbact 4x3
tggettatig gottooteat eletatooog oppatgotgg getggegean oppggaagae 540\,
egeteggace degacgeatg dadcattage aaggateatg getacactat emattecade 600
tttqqaqott totacatoon gotgotgoto atgotggtto totatgggog patattooga 660
gatgegeget teegeateeg caagaeggte aaaaaggtgg agaagaeegg ageggaeace 720
```

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ogocatygag batotosogo occynagodo aayaagagtig tigaatggaga yhiiggiggago 780
aggaictgga ggotgggogt ggagagoaag gotgggggtg ototytgogo maatggogog 840
gtgaggcaag gtgacgatgg ogoogoodtg gaggtgatog aggtgcacog agtgggcaac 90.)
tocasagage actigocici geodagegag getgqtecta eccettgige eneegecict 960
ttogagagga aaaatgagog baabgoogag gogaagogba agatggoobt gyboogagag 1920
agguagadag tgaagadgot gggoatbatb atgggoabot tbatkototg whggotgobb 1 940
ttothoatog tggotottgt totgopotto tgogagagoa getgopapat geboacotg 1240
ttyyjogoda taatoaatty gotgggotab todaactoto tgottaadoo ogtbatttad 1300
qcatactica acaaggacti toaaaaogog titaagaaga toattaagig taacticigo 1.000
goggoogdad ggggadgdad dodadddagd otgggtdddd aagatgagto otgdaddadd 1300
gobagotect cootggocaa ggacactica togtga
₹210 + 13
3311 · 1185
AND LO - DNA
 '213 - Artifictal Séquence
11220 -
-1223 - hugleotide sequence of beta3-AR-V2R chimera
+400 + 13
atgyntocyt gydotbacya yaabayotot ottyboodat gydegyadet (1867adeety 6)
pogodaata cogodaacad cagtgggotg coaggggtto cytgggagge gynnotagod 1.
ggggmastga tygogatygo yytyotygoa acaytyggay gaaacatgat 43\% ratayty 1\pi
godatogodi ggadtoogag abtobagado atgaddaadg tgttogtgad (1.990tggbb 24
gbagbegabe tygtgatygg abtebtggtg gtgbbgdbgg bggbbackt gybgbtgabt \delta C
iggadaatgga agtigggaga daatggatga gagatgigga dataggigga agtgatgigt 36%
gtgacegesa geategaaac estgtgeges etggeegtgg acegetaest ggetgtgace 4\%\%
aaccogotgo gttacggogo actggtcacc aagcgctgcg cooggacago tgtggtcctg 480
gtgtgggteg tgteggeege ggtgtegttt gegeedatea tgageeagtg gtggegegta 540
gaggnegaby begaggegea gegetyepab tobaabbegs gotgetytyb ottogobtob 6\%
ascat good addition good octoored groupottat accitedist to tog train 6\pi^{\circ}
-ctothograph abgogogygt tittogtgyty gotabycybb agotycydti ychydydygy 🐩
paguingggas gotitosgos agaggagtat enganggags egiogogoth thiquenneg
garanggtag ggaagtgaga taagaaagaa gyggtgaaag aatgaggaag yaxaaaagag 44\%
ogostootgo ototooggga adaoogggoo otgtgoacot tgggtotoat catgggoaco 90
terautotic gotggttgod stietticty godaacgigs igogogodsi ggggggddoc 900
totoragios eggypheggo titlocitged etgaäciggo taggitatgo baaliteigeb 10.00
This varies teathrapty engageesy gaettteges gegeettees in whattety 1\%36
right:Stight equalization displantines because the topose is an earth 2014;
typaccascy coagethate octggodaag gabactteat bytga
-211 - 14
· 311 · 1089
- 113 - DNA
Halls - Artificial Sequence
-1225-
<:22? - nucleotide sequence of Edgl-V2R chimera</pre>
-(4.00 + 1.4)
atggqgccca ccaggqtbcc gptggtbaag griftaccgca gribggtoto tuurtabgto 6
aastatgata toatogtoog grattamaad tamazgggaa agotgaatat magggggac 1. \Im
aangadaana qoattilaant maantiggtig ghyttimatti thatistgotig ittiaticatio 180
otgga mala a mingtimit got jannatt tiggaalappa aljaaattoba imiabolatg 240
tarrarinta tiqiraanut ggqoorotoa qarorgtogg bagyagtago htaracagot 300
```

aa eerahi iti irgi irggga baa waabataa aa mutbaathi irgii wagtigi gifii itgagglpha

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gaagggagta tgtttgtgge cetgtcagee teegtyttea gteteetege bategeeatt 420
gagogotata toacaatgot gaaaatgaaa otocacaacy ggagcaataa ottoogooto 430
ttootgotaa tragogorty otgggtrato trooteated tgggtggeet geetateatg 540
ggotggaact geatsagtgs getgtesags tysteeaseg tystgeegst etaceacaag 600
cactatates tettotgeas caeggiette astotgette tgetetecat egicationg 660
taotypagaa totaotoott yytpagyabt oygagobyob yobtyabytt brybaayaab 74\%
atttocaagg obagoogbag ototgagaag togotggogo tgotcaagab ogtaattato 790
qteetqageg tetteatege etgetgggea eegetettea teetgeteet getggatgtg 840
ggotycaagg tgaagacoty tgacatooto ttoagagogg agtacttoot ggtgttagot 900
gtgotbaact ooggbaccaa ooccatcatt tacactotga ocaacaagga gatgogtogg 960
geotteated ggateatgte etgetgeaag tgegeggeeg caeggggaeg caeeecacee 1020
ageotyggte decaagatga gtootgeace acegecaget detectigge haaggadact 1080
toatogtga
-:210 - 15
+1211 + 43
-1112 × PE.T
-0013 - Homo sapiena
-1400 \cdot 15
Ash Pro Ile Val Tyr Ala Phe Arg Ile Gln Lys Phe Arg Val Thr Phe
                                     10
Leu Lys Ile Trp Ash Asp His Phe Ard Cys Gir Pro Ala Pro Pro Ile
                                 2.5
Asp Glu Asp Leu Pro Glu Glu Arg Pro Asp Asp
        35
<2105-16
<2115 176
<2212> PRT
+:213 > Homo sapiens
-1400 \cdot 16
Asr. Pro Ile Ile Tyr Pro Cys Ser Ser Lys Glu Phe Arg Ala Phe Val
                                     10
Arg Ile Leu Gly Cys Glr. Cys Arg Gly Arg Gly Arg Arg Arg Arg Arg
Arg Arg Arg Leu Gly Gly Cys Ala Tyr Thr Tyr Arg Pro Trp Thr
                             40
Arg Bly Gly Ser Let Blu Arg Ser Gln Ser Arg Lys Asp Ser Let Asp
                         55
                 Oys Leu Ser Gly Ser Gin Arg Thr Lou Fro Jer Ala
Ser Pro Ser Ero Gly Tyr Leu Gly Arg Gly Ala Fro Pro Pr
                                     90
    Tys Ala Pne Pro Glu Trp Lys Ala Pro Gly Ala Leu Leu Ser Leu
                                 105
Pro Ala Pro Glu Pro Pro Gly Arg Arg Gly Arg His Asp Ser Gly Pro
Leu Phe Thr Phe Lys Leu Leu Thr Glu Pro Glu Ser Pro Gly Thr Asp
                         135
    130
Gly Gly Ala Ser Asn Gly Gly Cys Glu Ala Ala Ala Asp Val Ala Asn
                                         155
                    150
145
Gly Gln Pro Gly Phe Lys Ser Asn Met Pro Leu Ala Fro Gly
```

```
<210> 15
-:211> 29
CU12 - PRT
.213 · Homo sapiens
\pm 400 \cdot 17
Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala Phe
                                     10
                 10
Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys Arg Ile Val
            20
-21^{\circ} - 18
+111 + 29
· . l. · PPT
-11∃ - Hdman
+400 + 18
Asn Fro Val Ile Tyr Thr Ile Phe Asn Gln Asp Phe Arg Ala Phe
                                    10
Arg Arg Ile Leu Cys Arg Fro Trp Thr Glm Thr Ala Trp
            20
+210 + 19
111 31
< D12 PRT</pre>
-213> Human
+4000-19
Ash iro Val Ile Tyr Thr Val Phe Ash Gln Asp Phe Arg Pro Ser Phe
                                     10
Lys His Ile Leu Phe Arg Arg Arg Arg Arg Gly Phe Arg Gln
+316 + 20
- 211 - 105
-212 - PRT
-213 - Homo sapiend
1400 - 20
Ash Pro Ile Ile Tyr Cys Arg Ser Pro Aar Phe Arg Lys Ala Ebec Un
Gly Leo Leo Cys Cys Ala Arg Arg Ala Ala Arg Arg Arg His Ala Thr
His Gly Asp Arg Pro Arg Ala Ser Gly Cys Leu Ala Arg Pro Hly Pro
                             40
Pro Pro Ser Pro G.y Ala Ala Ser Asp Asp Asp Asp Asp Asp Val Val
                         55
Bly Ala Thr Pro Pro Ala Arg Leu Leu Glu Pro Trp Ala Gly Tys Asn
Bly Gly Ala Ala Ala Asp Ser Asp Ser Ser Led Asp Gld Fro Cys Arg
ard Mly abe Alm Dar Mlu Ber Lys Val
```

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4210 - 21
<21115 42
S212 - PRT
4.213 > Homo sariens
-400: 21
Asr. Pro Leu Ile Tyr Cys Arg Ser Pro Asp Phe Arg Ile Ala Phe Gln
                                    10
Hiu Leu Leu Cys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Gly Asn Gly
                                25
Tyr De: Ser Ash Gly Ash Thr Gly Glu Gln Ser Gly Tyr His Val Glu
                            40
Glr. Glu Lys Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Th: Glu
                       5.5
Asp Phe Val Gly His Gln Gly Thr Val Pro Ser Asp Asn Ile Asp Ser
                   7.0
Gln Gly Arg Asn Cys Ser Thr Asn Asp Ser Leu Leu
-211 \cdot 120
+212> FRT
-213 - Homo sapiens
-400-12
Asr. Fre Ile Ile Tyr Ala Phe Asn Ala Asp Phe Arg Lys Ala Phe Ser
                                     10
Thr let Leu Gly Cys Tyr Arg Leu Cys Pro Ala Thr Asn Asn Ala Ile
                                25
Glu Thr Val Ser Ile Asn Asn Asn Gly Ala Ala Met Phe Ser Ser His
His Gl. Pro Arg Gly Ser Ile Ser Lys Glu Cys Ash Leu Val Tyr Leu
The Pro His Ala Val Gly Ser Ser Glu Asp Leu Lys Lys Glu Glu Ala
                    70
65
Ala Gly Ile Ala Arg Pro Leu Glu Lys Leu Ser Pro Ala Leu Ser Val
            9.5
                                    90
Ile Lei Asp Tyr Asp Thr Asp Val Ser Leu Glu Lys Ile Gln Fr. Ile
                                105
Inr the Ash thy the Big Fre The
-1210 + 23
<211 ⋅ 22
1212 · PRT
H213 - Human
<409h 23
Ash Fro Ile Ile Tyr Thr Thr Phe Ash Ile Blu Phe Arg Lyr Ala Phe
Led Lys Ile Led His Cys
            20
```

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<2105 24
<211: 22
+12121: PRT
Human
<400L 24
Asn Fro Val Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala Phe
           5
                                   10
1
Leu Lys Ile Leu Ser Cys
            20
·1110 - 15
-0.13 - Human
400% 15
Ash Fro Val Ile Tyr Thr Val Phe Ash Ala Glu Phe Arg Ash Val Phe
ì
Arg Lys Ala Leu Arg Ala Cys Cys
<110 \cdot 16
111 113
<212> PRT
+213> Human
· 100 · .6
Asn Fro Val Ile Tyr Ala Phe Asn Ala Asp Phe Gln Lys Val Phe Ala
                                    10
G.n Leu Leu Gly Cys Ser His Phe Cys Ser Arg Thr Pro Val Glu Thr
                                25
Val Ash Ile Ser Ash Glu Leu Ile Ser Tyr Ash Gln Asp Ile Val Fhe
His Lys Glu ile Ala Ala Ala Tyr Ile His Met Met Pro Ash Ala Val
                        55
                                            60
Thr Pro Gly Ash Ard Glu Val Asp Ash Asp Glu Glu Glu Gly Pro Phe
Asp Arg Met Phe Gln Ile Tyr Gln Thr Ser Pro Asp Gly Asp Ent Usl
                35
Ala Glu Ser Val Trp Glu Leu Asp Cys Glu Gly Glu Ile Ger in a Asq
Lys lle Thr Pro Phe Thr Pro Ash Gly Phe His
<310 + 27
<211 - 47
<212 → PRT
<213> Homo sariens
4
Ash Eri Met Tys Tyr Ala Tet Tys Ash Lys Ala Ehe Arg Asp Thr Ehe
```

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Arg Leu Leu Leu Cys Arg Trp Asp Lys Arg Arg Trp Arg Lys 110
Pro Lys Arg Pro Gly Ser Val His Arg Thr Pro Ser Arg Gln Tys
                             40
-1210 - 28
+:211* 31
-212 · FRT
1313 Homo sapiens
-1100 - 28
Ash Pro Ala Cys Tyr Ala Leu Cys Ash Ala Thr Phe Lys Lys Thr Phe
                                     10
Lys His Leu Leu Met Cys His Tyr Lys Asn Ile Gly Ala Th: A::
- 11(:- 29
-:11: 51
+ 2120 FF.T
·T15: Homo sapiens
· 4000- 29
Ash Fro Val Cys Tyr Ala Leu Gys Ash Lys Thr Phe Arg Thr Thr Fhe
Lys Met Leu Leu Cys Gln Cys Asp Lys Lys Arg Arg Lys Gln
            20
                                 25
Gln Tyr Gln Gln Arg Gln Ser Val Ile Phe His Lys Arg Ala Pro Glu
                           40
Gin Ala Leu
   5.0
-1.11(y- 30
·::111 · 31
-1.112 · PET
-M13: Homo sapiens
-(400 - 30
Ash Pro Ala Cys Tyr Ala Leu Cys Ash Ala Thr Phe Lys Lys Thr Phe
Arg Bi. Leu Leu Leu Cys Fin Tyr Arg Asn lle Sly Thr Als Ars
H210 - 31
-:211> 42
<.1125 FRT
<213> Artificial Sequence
4.3235
<223> n5 muscarinic receptor
K4005 41
Ash Pro Ile Cys Tyr Ala Leu Cys Ash Arg Thr Phe Arg Lys Thr Ibe
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Lys Met Leu Leu Cys Arg Trp Lys Lys Lys Val Eli Elu Lys
          4.2
                                2:
Leu Tyr Trp Gln Gly Asn Ser Lys Leu Pro
        35
<210 - 32
<211 + 24
<212 · PRT
-213 · Homo sapiens
-1400 - 32
Ash Pro Val Ile Tyr Ala Tyr Phe Ash Lys Asp Phe Gln Ash Ala Phe
                                10
Lys by Tie lie Lys Tys Lys Phe
HI210H 33
-1211x 16
-1.127 FET
· 113 - Homo sapiens
#4001- E3
Aan Erd Ile Ile Tyr Thr Met Ser Ash Glu Asp Ehe Lys (in Als Eng
1
                    10
                5
His Lys Leu Ile Arg Phe Lys Cys Thr Ser
· 210:- 34
-111- 14
+112> EFT
+113/ Homo sapiens
+400.+ 14
Ash Pro Leu Leu Tyr Thr Ser Phe Ash Glu Asp Phe Lys Leu Ala Phe
                                10
Lys Lyk Leu Ile Arg Cys Arg Glu
-1.11
+..11 - -7
212 - FRT
-.139 Artificial Sequence
. 203
.235 .lfactory receptor 6A1
- 400> -5
Ash Pro lie lie Tyr Tys Leu Arg Ash Sin Siu Val Lys Arg Ala Deu
Dys Dys The Lou His Lou Typ Olm His Olm Asp Ert Asp Er Lys Lys
Gly Jer Arg Ash Val
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<210> 36
\pm 211 \pm 27
-1.112 + FRT
H.213 - Artificial Sequence
·120L
+223. olfactory receptor 2C1
-1400x 36
Ash Pro Leu Ile Tyr Thr Leu Arg Ash Met Glu Val Lys Gly Ala Leu
                                     10
Arg Arg Leu Leu Gly Lys Gly Arg Glu Val Gly
·:210:- .:-7
. 211: €2
+2120 ERT
·213: Homo sapiens
· 4000 37
Ash Fro Leu Phe Tyr Gly Fhe Leu Gly Lys Lys Phe Lys Arg Tyr Phe
Leu Oln Leu Leu Lys Tyr lle Pro Pro Lys Ala Lys Ser His Ser Asn
Leu Ser Thr Lys Met Ser Thr Leu Ser Tyr Arg Pro Ser Asp Asn Val
                            40
Ser Ser Ser Thr Lys Lys Pro Ala Pro Cys Phe Glu Val Glu
                        5.5
·:10 - 38
+.111: 50
+.12: FRT
-7.15: Homo sapiens
+4001-38
Ash ird Phe Leu Tyr Cys Phe Val Gly Ash Ar; The Gln Gln Lys Leu
                                     10
Arg fer Val Phe Arg Val Pro Ile Thr Trp Leu Sin Gly Lys Arg Glu
Der Met Ser Typ And Lyp der Ser der Lei Anis Aus Wit All This Ebe
Mal Jer
  50
H1110 - 33
4211- 51
K212> FRT
<213> Fomo sapiets
Ash Fro Leu Ile Tyr Ala Fhe Ile Bly Bln Lys Phe Ary How Bly Leu I
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Leu Lys Ile Leu Ala ile His Gly Leu Ile Ser Lys Asp Ser Leu Pro
                               25
Lys Asp Ser Arg Pro Ser Phe Val Gly Ser Ser Ser Gly His Thr Ser
        35
Thr Thr Leu
    50
<210 ⋅ 40
∹211 • 6"
<212> PRT
-1.113 Artificial Sequence
.1.120 -
-1.23 - cx3c shemokine resenter 1 (-x3-r1) (fractalkine)
     redeptor
436-46
Ash Pro Leu Ile Tyr Ala Phe Ala Gly Glu Lys Phe Arg Arg Tyr Leu
1
Tyr His Leu Tyr Gly Lys Cys Leu Ala Val Leu Cys Gly Arg Ser Val
           20
                               25
His Val Asp Phe Ser Ser Ser Glu Ser Gln Arg Ser Arg His Gly Ser
                           40
Val Leu Ser Ser Asm Phe Thr Tyr His Thr Ser Asp Gly Asp Ala Leu
                       55
  5.0
Leu Leu Leu
65
·1.10: 41
H1115 59
KIDIDI PET
HU130 Human
41:00:41
Ash Fro Ile Leu Tyr Ash Leu Val Ser Ala Ash Phe Arg His Ile Fhe
Lou Ala Thr Leu Ala Cys Leu Cys Pro Val Trp Arg Arg Arg Lys
Arg Fro Ala Phe Ser Arg Lys Ala Asp Ser Val Ser Ser Asr. His Thr
                           40
Lwu Jer Ser Ash Ala Thr Arg Slu Thr Led Tyr
1.10 - 42
4.11: - 107
. 11. PRT
4.13 · Artifitial Sequence
*4009 42
Ash Pro II.e II.e Tyr Tyf Tys Lêu Ash Asp Ary Fhe Ard Lou Boy The
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## 033072-026.ST25

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Lys His Ala Phe Arg Cys Cys Pro Phe 11e Ser Ala Gly Asp Tyr Glu 20 31  
Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Cer Val 35  
Tyr Lys Val Ser Arg Leu Glu Thr Thr 11e Ser Thr Val Val Gly Ala 50  
His Glu Glu Glu Pro Glu Asp Gly Pro Lys Ala Thr Pro Ser Ser Leu 70  
Asp Leu Thr Ser Asn Cys Ser Ser Arg Ser Asp Ser Lys Thr Met Thr 85  
Glu Ger Phe Ser Phe Ser Ser Asn Val Leu Ser 105  
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+110+43 +111+50 +112+ PRT +113+ Homo sapiens

+400"+ 43

+210> 44 +211> 83 +212> PET +713> Human

<4000 45</p>
Ash Pro Trp Ile Tyr Met Leu Phe Thr 31y His Leu Phe His Hu Leu

```
1
Val Gin Arg Phe Leu Cys Cys Ser Ala Ser Tyr Leu Lys Gly Arg Arg
Leu Gly Glu Thr Ser Ala Ser Lys Lys Ser Asn Ser Ser Ser Phe Val
                             40
Lou Gor His Arg Ser Ser Ser Gln Arg Ser Cys Ger Gln Fr. Der Ihr
Ala
to D
-210 - 46
<211 · 75
+212 + PRT
.13 · Homo sapiens
+400 + 46
Ash Ero Val Leu Tyr Ser Leu Met Ser Ser Arg Fhe Arg Glu inn Fhè
Glm Glu Ala Leu Cys Leu Gly Ala Cys Cys His Arg Leu Arg Pro Arg
His Fer Ser His Ser Leu Ser Arg Met Thr Thr Gly Ser Thr Lea Cys
                             4.0
Asp Val Gly Ser Leu Gly Ser Trp Val His Pro Leu Ala Gly Asr. Asp
                        55
Gly Fro Glu Ala Gln Gln Glu Thr Asp Pro Ser
1.5.
                     70
< 210: 47
· 1.11: 62
·112: PET
+113 Hcmc sapiens
+400 - 47
Awn Fro Leu Val Tyr Cys Phe Met His Arg Arg Phe Arg Gln Ala Cys
Leu Glu Thr Cys Ala Arg Cys Cys Pro Arg Pro Pro Arg Ala Arg Pro
Ang Ala Leu Pro Asp Glu Asp Pro Pro Thr Pro Per Ile Ala Jer Leu
+.110 + 45
- 111 - 82
-.:12 - PR.T
<113 Homo sapiens
< 400 + 48
Ash Pro Leu Val Tyr Ala Leu Ala Ser Arg His Phe Arg Ala Ara Phe
Arg Arg Leu Trp Ero Tys Sly Arg Arg Arg Arg His Arg Ala Arg Arg
Ala Lei Arg Ari Mal Arg Pro Ala Son Ser Bly Pro Pro Bly Tys Pro
        3.5
```

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Gly Asp Ala Arg Pro Ser Gly Arg Leu Leu Ala Gly Gly Gly Gln Gly
Pro Glu Fro Arg Glu Gly Pro Val His Gly Gly Glu Ala Ala Arg Gly
Pro Glu
<210 > 49
< 211 \cdot 76
+312 + PRT
-213 · Human
4409 - 49
Ash Pro Ile Ile Tyr Thr Leu Thr Ash Lys Glu Met Arg Act Act the
The Arg Ile Met Ser Cys Cys Lys Cys Fro Ser Gly Asp Sor Ala Gly
                                 25
Lys Phe Lys Arg Pro Ile Ile Ala Gly Met Glu Phe Ser Arg Jer Lys
                            40
Ser Asp Asn Ser Ser His Pro Gln Lys Asp Glu Gly Asp Asn Pro Glu
                        5.5
Thr Ile Met Ser Ser Gly Asn Val Asr. Ser Ser Ser
· 2101- 50
· 111-- 86
·2127 PFT
· 113 · Homo sapiens
44000 50
Ash Pro Ile Ile Tyr Ala Leu Arg Ser Lys Asp Leu Arg His Ala Phe
Arg Jer Met Phe Pro Ser Cys Glu Gly Thr Ala Gin Pro Lei Agy Ash
Ser Met Gly Asp Ser Asp Cys Leu His Lys His Ala Ash Ash Ala Ala
                             40
Mer Val His Arg Ala Ala Glu Ser Cys Ile Lys Ser Thr Val Lys Ile
Ala Lys Val Thr Met Ser Val Ser Thr Asp Thr Ser Ala Glu Ala Leu
·..*10 · 51
4211 + 59
HO12 - FRT
-1213 - Human
4400 / 51
Ash Pro Val Leu Tyr Ala The Leu Asp Glu Ash Phe Lys Ary Tys the
Arg Sin Leu Cys Arg Lys Pro Cys Sly Arg Pro Asp Pro Ser Jer Phe
Ser Arg Pro Arg Glu Ala Thr Ala Arg 31% Arg Mal Thr Ala 198 Thr
        35
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Fro Ser Asp Gly Pro Gly Gly Gly Arg Ala Ala

50 55

<:210 > 52
<:211 - 58
<:212 - PRT</pre>

H213 - Human

-1400 - 52

Asp Fro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala 1 5 10 15

Lys Asr. Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln 20 25 36

Wal Fer Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Ser Ty: Ger 35 40 40

Ser er Ser Thr Thr Val Lys Thr Ser Tyr

-110 - 53

.111 - 66

· [12 · FRT

 $\cdot$  113  $\cdot$  Fat

+400 + 53

Ash Gly Glu Val Gln Ala Glu Leu Arg Arg Lys Trp Arg Arg Trp His 1 5 10 10

Leu Glr. Gly Val Leu Gly Trp Ser Ser Lys Ser Gln His Pro Trp Gly 20 25 30

Gly Ser Asn Gly Ala Thr Cys Ser Thr Gln Val Ser Met Leu Thr Arg 40 45

Val Ser Pro Ser Ala Arg Arg Ser Ser Ser Phe Gln Ala Glu Val Ser 50 55 60

Leu Tal

 $C_{j} \subseteq C_{j}$ 

 $4210 \pm 54$ 

311 - 93

-0.11.2 · DNA

- 213 - Human

44354 84

proceedings gradure sace diagoning to be caused a general contract that is a contract to the contract of the

 $\pm 310 - 55$ 

311 - 114

-1212 - DNA

-:213 - Human

-1400 - 55

geggeegean gyggangsab becauseage stgygteses aagatgagto styrascase 60 geoagethit brotquisaa quaraettea teytgaayat stoogiggto tasa 114

. 21 - 5 - 5 -

```
<2135 PF.T
<213 · Artificial Sequence</pre>
-1.22 1 +
HD23+ carboxy terminus of modified GPCR
Ala Ala Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gin Asp Glu
                                    10
Ser Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
\pm 210 \pm 57
·::::: 3.1
HILL PRIT
Ell: Artificial Sequence
-111: carboxyl-terminal tail of V2R
+14(i + 57
Cys Ala Arg Gly Arg Thr Pro Prc Ser Leu Gly Pro Gln Asp Glu Ser
                                    10
Cys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Thr Ser Ser
                                 25
<210 · 58
F1115 20
.010> PFT
<113> Artificial Sequence
12.5 (**)
01227 V2R mutant receptor
414. - 58
Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gln Asp Gld Ser
Cys Thr Thr Ala
            20
tolor PAT
HULL: Artificial Sequence
+333 - V2R mutant receptor
<47.72 59
Cyn Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gln Asr Glu Cer
                                    10
Cys Thr Thr Ala Ala Ala Ala Leu Ala Lys Asp Ala Ala Ala
```

```
<21 0 61
<211 > 30
<212 \cdot PRT
3213 · Artificial Sequence
42200 -
+223 + V2R mutant receptor
+140(0.4 60
Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Glm Asp Glu Ser
       5 10
lys Thr Thr Ala Ser Ser Ser Leu Ala Lys Asp Ala Ala Ala
                   25
-.14 - €1
+2110 30
- 1120 FET
-113: Artificial Sequence
٠. ا ا ا ا ا
+223: V2R mutant receptor
· 4000 61
Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Gl: Ay Gla Ser
                      10
: 5
Cys Thr Thr Ala Ala Ala Ala Leu Ala Lys Asp Thr Ser Ser
                      25
+110> 62
· 111: 30
+1110 \times EFT
-1135 Artificial Sequence
· 13(...
+113. keta-2AR mutant receptor
170 + 62
Tys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly Pro Glt Asj Glu Ser
       5
                      10
tys Thr Thr Ala Ala Ala Ala Leu Ala Lys Asp Thr Jer Jer
           63
-.110 € 3
 1111-73
-1012 - ERT
F1113 / Artificial Sequence
<!d23> carboxyl-terminal fail of beta-2AB
Cys Leu Arg Arg Sor Ser Leu Lys Ala Typ Gly Ast Gly Typ Ser Cer
```

## 033072-026.3725

```
Ash Gly Ash Thr Gly Glu Gin Ser Gly Tyr His Val Glu Win Flu Lys
Glu Asn Lys Leu Leu Cys Glu Asp Leu Pro Gly Thr Glu Asp Phe Val
        35
                             40
Gly His Gln Gly Thr Val Fro Ser Asp Ash He Asp Ser Gln Gly Arg
Asn Cys Ser Thr Asn Asp Ser Leu Leu
10 €4
-0.11 \pm 83
+112x+ PRT
-713 Artificial Sequence
201
+1113 beta-2AR mutant receptor
+400. €4
Cys Leo Arg Arg Ser Ser Leo Lys Ala Tyr Gly Asn Gly Tyr Ser Ser
Asr. Gly Asn Thr Gly Glu Gln Ser Gly Tyr His Val Glu Gln Hiu Lys
            20
Glu Asn Lys Leu Cys Glu Asp Leu Pro Gly Thr Glu Asp The Val
        35
                            4 0
May his Glm Gly Thr Val Pro Ser Asp Asm Ile Asp Ser Glm Bly Ara
                        5.5
Asn Cys Ser Thr Asn Asp Ser Leu Leu Ser Ser Ser Leu Ala Lys Asp
                    70
                                        75
Thr Ser Ser
-110% 65
#111. €C
+1.12(+ PET
1.13 Artificial Sequence
-1206
<:::3+ beta-2AR mutant receptor</pre>
<400 - 65
Dys Leu Arg Arg Ser Ser Leu Lys Ala Tyr Hy Ash Hy Tyr Jer Jer
Ash Bly Ash Thr Cer Cer Çer Leu Ala Lyc Asp Thr Cer Cer
            612
· .: * . 66
11111 - 51
ROLL PRT
<313  Artificial Sequence</pre>
<232 carboxyl-terminal fail of V2R</pre>
<4170 6€
```

```
Ash Fro Trp Ile Tyr Ala Ser Phe Ser Cer Cer Val Ser Ser Glu Leu
,
Arg Ser Leu Leu Cys Cys Ala Arg Gly Arg Thr Pro Pro Ser Leu Gly
          2:0
                                25
to Gln Asp Glu Ser Cys Thr Thr Ala Ser Ser Ser Lou Ala Lys Asp
Thr Jer Ser
    - 0
·210 €7
·1211 - 51
HI 12 · FRT
·113 · Artificial Sequence
+22% reseptor mutant
-14001- 67
Asr. Fro Trp Ile Tyr Ala Ser Phe Ser Ser Ser Val Ser Ser Slu Leu
And Ser Leu Leu Cys Cys Ala Ang Gly Ang Thr Pro Pro Fer Leu Gly
Pro Gln Asp Glu Ser Cys Thr Thr Ala Ser Ala Ala Ala Ala lys Asp
                            40
Thr Ser Ser
   5.0
<210> 68
.:211: 52
HILLS FRT
Hill: Artificial Sequence
-122
HL23 - receptor mutant
-:401-- 68
Am Pro Trp Ile Tyr Ala Ser Phe Ser Ser Ser Val Ser Ser Wid Leu
                                    1 🗥
Ang Jer Leu Leu Cys Gys Ala Ang Gly And Thr Pro Pro Per Lea Gly
    20
Pro Hin Asp Glu Ser Cys Thr Thr Ala Ter Jer Jer Lau Ala Ly - Aq
                            40
 35
Imr Ala Ala Ala
    70
<310 ⋅ 69
<211 → 65
:212 · PRT
<213 - Artificial Sequence
<2239 zazbowyl-twrminal tabl : NTR-1
111112
```

```
Ash Pro Ile Leu Tyr Ash Leu Val Ser Ala Ash Fhe Ary Gin Val Fhe
1
                                      10
Leu Ser Thr Leu Ala Cys Leu Cys Pro Gly Trp Arg His Ard Arg Lys
             20
Lys Arg Pro Thr Phe Ser Aru Lys Pro Ash Ser Met Ser Ser Ash His
Ala the Ser Thr Ser Ala Thr Arg Glu Thr Leu Tyr
<310 - 70
5.111 × 60
-2.212 + PRT
<213 - Artificial Sequence</p>
·:220 ·
+223 · receptor mutant
1100 70
Aun Pro Ile Leu Tyr Asn Leu Val Ser Ala Asn Phe Arg Glr. Val Phe
Leu der Thr Leu Ala Cys Leu Cys Pro Gly Trp Arg His Arg Arg Lys
Lys Ard Pro Thr Phe Ser Arg Lys Pro Asn Ser Ala Ser Ala Ala His
                             4.0
Ala The Ser Thr Ser Ala Thr Arg Glu Thr Leu Tyr
32100-71
-2111 €C
<21121 FF.T
<:213: Artificial Sequence</pre>
11111000
HIII3 - receptor mutant
4 0 11
Ash Pro Ile Leu Tyr Ash Leu Val Ser Ala Ash Phe Arg Gir. Val Phe
                                      10
Lett for Thr Lett Ala Cys Lett Cys Pro Gly Trp Ar; His At; Ary Lys
        20
Lys Arr Fro Thr Fhe Ser Arg Lys Pru Asn Ser Met Ser Jer Ash His
Alashr Jer Ala Ala Ala Inn Ang Wil The Leu Tyr
1.110 - 12
4211 - 65
<212- PRT
<213 · Artificial dequence
5220 ·
%223> carbuxyl-terminal tail it %TR
<4117
```

```
Ash Pro Trp Hie Tyr Met Leu Phe Thr Gly His Leu Phe His Hu Leu
                                    10
Val Gln Arg Phe Leu Cys Cys Ser Ala Ser Tyr Leu Lys Gly Arg Arg
                                25
Leu Gly Glu Thr Ser Ala Ser Lys Lys Ser Asn Ser Ser Ser Etc. Va
                           4.0
Leu Ser His Ard Ser Ser Ser Gln Ard Ser Cys Ser Gln Pro Ger Thr
Ala
55
-1.110:- 73
-1711: 65
SULLEY PRT
· 13: Artificial Sequence
·1220:
HM230 receptor mutant
-1400: 73
Ash Pro Trp Ile Tyr Met Leu Phe Thr Gly His Leu Phe His Elu Leu
Val Gln Arg Phe Leu Cys Cys Ser Ala Ser Tyr Leu Lys Gly A:: Ala
                                25
            20
Ala Ala Ala Thr Ser Ala Ser Lys Lys Ser Asn Ser Ser Ser Ethe Val
                            40
 35
                                                45
Leu Ser His Arg Ser Ser Ser Gln Arg Ser Cys Ser Gln Pro Ser Thr
               55
Ala
ri E.
·11100 74
-1211:- 65
H212H PRT
3213 - Artificial Sequence
·:2201
RL23% receptor mutant
:400 - 74
Asn Pro Trp Ile Tyr Met Leu Phe Thr Sly His Leu Phe His Il: Leu
Val Uln Arg Fhe Led Cys Cys Cer Ala Cer Tyr Led Lys 187 Ard Ard
                                25
Leu Gly Glu Thr Ser Ala Ala Ala Ala Ser Ash Ser Ser Ser End Val
                         40
Leu Jer His Arg Ser Ser Ser Gln Arg Ser Cys Ser Gln Pro Ser Thr
                        55
Ala
65
7210% 19
72117 75
```

```
<213> Artificial Sequence
<2220
KUM3 - reseptor mutant
44 6 - 75
Ash Pro Trp Ile Tyr Met Leu Phe Thr Gly His Leu Phe His Glu Leu
                                     1.0
Wal Gln Arg Phe Leu Cys Cys Ser Ala Ser Tyr Leu Lys Gly Arg Arg
Leu Gly Glu Thr Ser Ala Ser Lys Lys Ser Asn Ser Ser Ser Fhe Val
     3.5
                             40
Leu Jer His Arg Ala Ala Ala Gln Arg Ser Cys Ser Gln Fro Jer Thr
                         5.5
A \perp \alpha
+5.5
<110 - 76</pre>
4111 \pm 105
4012 - PRT
HILLS - Artificial Sequence
HP13 · darboxyl-terminal tail of SPR
\pm 1400 - 76
Asn Fro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Gly Phe
Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu
Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Val Tyr
                             40
Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly A.a His
                         55.
Giu Giu Siu Pro Giu Siy Pro Lys Ala Thr Pro Ser Ser Leu lyw Leu
This Jer Ash Cys Ser Ser Ang Ser Asp Ser Lys Thr Mot Thir 100 Ser
                8.5
Phe Ser Phe Ser Ser Asn Val Leu Ser
            100
. 2111 - 77
 311 - Es
 LIL · FRT
<213 - Artificial Sequence
4220 -
*223 · receptor mutant
4400 - 17
Ash Pro lie Tie Tyr Cys Tys Leu Ash Asp Arg The Arg 182 Mg Hib-
lys His Ala The Arg Cys Cys Pro The 110 Jer Ala 31y Arg Tyr Si:
```

Bly Let Blu Met Lys Per Thr Arg Tyr Let Bln Thr Bln Bly Wal Tyr

```
35
                              40
Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr Val Val Gly Ala His
                         55
Glu Glu
65
+210 + 78
-211 - 44
-212 + PET
<213 > Artificial Sequence
4220 s
<223 · receptor mutant
4 17 - 79
Asr. Fro Ile Ile Tyr Cys Cys Leu Asn Asp Arg Phe Arg Leu Hly Phe
                                      10
Lys His Ala Fhe Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu
                                 25
Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr
- 110a - 79
+211.- 20
-2173 PP.T
<213> Artificial Sequence
<220>
<223> receptor mutant
-466: 79
Ash Fro Ile Ile Tyr Cys Cys Leu Ash Asp Arg Phe Arg Leu Cly Phe
Lys His Ala Phe
            2.0
·::: • +(
. 211 - 89
. III. . BET
- Ll - Artificial Sequence
121
-%.ids - receptor mutant
4400× 30
Ash Pro Ile Ile Tyr Cys Cys Leu Ash Asp Arg Phe Arg Leu Gly Phe
Lys His Ala Phe Arg Cys Cys Pro Phe Ile Ser Ala Gly Asp Tyr Glu
317 Leu Glu Met Lys Ser Thr Arg Tyr Leu Glm Thr Ala Ala Val Ala
                             40
Ala Val Ser Arg Leu Glo Thr Thr Ile Ser Thr Val Val Gly Ala His
    5<sub>m</sub>C
Glu Glu Glu Fre Gl:
```

65

20 25 30 Gly Leu Glu Met Lys Ser Thr Arg Tyr Leu Gln Thr Gln Gly Val Tyr 35 40 45

Lys Val Ser Arg Leu Glu Thr Thr Ile Ser Thr Val Ala Gly Ala Ala 50 55 60

Glu Glu Glu Pro

65